

SEQUENCE LISTING

<110> TAKAIWA, MIKIO

OKUDA, MITSUYOSHI

SAEKI, KATSUHISA

KUBOTA, HIROMI

HITOMI, JUN

KAGEYAMA, YASUSHI

SHIKATA, SHITSUW

NOMURA, MASAFUMI

<120> ALKALINE PROTEASE

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<141> 2000-04-06

<150> PCT/JP98/04528

<151> 1998-10-07

<150> JP 9-274570

<151> 1997-06-08

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Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	Asn	Glu		
			515				520				525						
tcc	agt	gcc	cta	tca	act	agc	caa	aaa	gcg	aca	tat	acc	ttt	act	gca		1632
Ser	Ser	Ala	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Thr	Phe	Thr	Ala		
			530			535					540						
acg	gcg	ggc	aag	cca	ttg	aaa	atc	tcc	ctg	gta	tgg	tcg	gat	gcc	cct		1680
Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	Asp	Ala	Pro		
					550				555					560			

gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc	1728
Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val	
565 570 575	

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca	1776
Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala	
580 585 590	

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt	1824
Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe	
595 600 605	

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat	1872
Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr	
610 615 620	

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa	1920
Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn	
625 630 635	

<210> 4

<211> 639

<212> PRT

<213> Bacillus sp.

<400> 4

Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile
1 5 10 15

Leu Ser Thr Val Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr
20 25 30

Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly
35 40 45

Phe Ser Lys Gln Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
50 55 60

Glu Asn Val Lys Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val
65 70 75 80

Pro Ala Asn Asn Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu
85 90 95

Glu Glu Thr Lys Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp
100 105 110

Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln
115 120 125

Ser Lys Val Arg Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
130 135 140

Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr
145 150 155 160

Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val
165 170 175

Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp
180 185 190

Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
195 200 205

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
210 215 220

Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
225 230 235 240

Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
245 250 255

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
260 265 270

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn
275 280 285

Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
290 295 300

Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
305 310 315 320

Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
325 330 335

Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
340 345 350

Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
355 360 365

Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
370 375 380

Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
385 390 395 400

Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
405 410 415

Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile
420 425 430

Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn
435 440 445

His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro
450 455 460

Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn
465 470 475 480

Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala
485 490 495

Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp
500 505 510

Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu
515 520 525

Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala
530 535 540

Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro
545 550 555 560

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
565 570 575

Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
580 585 590

Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
 595 600 605

Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
 610 615 620

Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
 625 630 635

<210> 5

<211> 1923

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)..(1923)

<400> 5

atg aga aag aag aaa aag gtg ttt tta tct gtt tta tca gct gca gcg	48
Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala	
1 5 10 15	

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg	96
Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg	
20 25 30	

aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa	144
Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Asp Ala Lys	
35 40 45	

ggg ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa	192
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu	
50 55 60	

tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca	240
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr	
65 70 75 80	

gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att	288
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile	
85 90 95	

tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc	336
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu	
100 105 110	

gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val 115 120 125	384
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr 130 135 140	432
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser 145 150 155 160	480
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu 165 170 175	528
gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn 180 185 190	576
gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp 195 200 205	624
gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly 210 215 220	672
ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp 225 230 235 240	720
aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile 245 250 255	768
act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn 260 265 270	816
ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr 275 280 285	864
aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met 290 295 300	912
gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu 305 310 315 320	960
ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp 325 330 335	1008
gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp 340 345 350	1056

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat	1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn	
355 360 365	
gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat	1152
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn	
370 375 380	
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct	1200
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser	
385 390 395 400	
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg	1248
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro	
405 410 415	
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc	1296
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe	
420 425 430	
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg	1344
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala	
435 440 445	
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca	1392
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr	
450 455 460	
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa	1440
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys	
465 470 475 480	
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att	1488
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile	
485 490 495	
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga	1536
Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly	
500 505 510	
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac	1584
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn	
515 520 525	
gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act	1632
Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr	
530 535 540	
gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc	1680
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala	
545 550 555 560	
cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt	1728
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu	
565 570 575	
gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act	1776
Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr	
580 585 590	

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta	1824
Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val	
595 600 605	

ttt att aat gca cca caa agc ggg acg tat aca att gag gta cag gct	1872
Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala	
610 615 620	

tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att gtg aat	1920
Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn	
625 630 635 640	

taa	1923
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<210> 6

<211> 640

<212> PRT

<213> Bacillus sp.

<400> 6

Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
1 5 10 15

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
20 25 30

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
35 40 45

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
50 55 60

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65 70 75 80

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
85 90 95

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
100 105 110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
115 120 125

Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
130 135 140

Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145 150 155 160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
165 170 175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
180 185 190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
195 200 205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
210 215 220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225 230 235 240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
245 250 255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
260 265 270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
275 280 285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
290 295 300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305 310 315 320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
325 330 335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
340 345 350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
355 360 365

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
370 375 380

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385 390 395 400

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
405 410 415

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
420 425 430

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
435 440 445

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
450 455 460

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465 470 475 480

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
485 490 495

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
500 505 510

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
515 520 525

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
530 535 540

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545 550 555 560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
565 570 575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
580 585 590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
595 600 605

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
610 615 620

Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn
625 630 635 640

<210> 7

<211> 1923

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1) .. (1923)

<400> 7

atg	aga	aag	aag	aaa	aag	gtg	ttt	tta	tct	gtt	tta	tca	gct	gca	gcg	48
Met	Arg	Lys	Lys	Lys	Lys	Val	Phe	Leu	Ser	Val	Leu	Ser	Ala	Ala	Ala	
1				5					10					15		

att	ttg	tcg	act	gtt	gcg	tta	agt	aat	cca	tct	gca	ggg	ggg	gca	agg	96
Ile	Leu	Ser	Thr	Val	Ala	Leu	Ser	Asn	Pro	Ser	Ala	Gly	Gly	Ala	Arg	
			20					25					30			

aat	ttt	gat	ctg	gat	ttc	aaa	gga	att	cag	aca	aca	act	gat	gct	aaa	144
Asn	Phe	Asp	Leu	Asp	Phe	Lys	Gly	Ile	Gln	Thr	Thr	Thr	Asp	Ala	Lys	
		35					40					45				

ggg	ttc	tcc	aag	cag	ggg	cag	act	ggg	gct	gct	gct	ttt	ctg	gtg	gaa	192
Gly	Phe	Ser	Lys	Gln	Gly	Gln	Thr	Gly	Ala	Ala	Ala	Phe	Leu	Val	Glu	
	50					55					60					

tct	gaa	aat	gtg	aaa	ctc	cca	aaa	ggg	ttg	cag	aag	aag	ctt	gaa	aca	240
Ser	Glu	Asn	Val	Lys	Leu	Pro	Lys	Gly	Leu	Gln	Lys	Lys	Leu	Glu	Thr	
65					70					75					80	

gtc	ccg	gca	aat	aat	aaa	ctc	cat	att	atc	caa	ttc	aat	gga	cca	att	288
Val	Pro	Ala	Asn	Asn	Lys	Leu	His	Ile	Ile	Gln	Phe	Asn	Gly	Pro	Ile	
				85					90				95			

tta	gaa	gaa	aca	aaa	cag	cag	ctg	gaa	aaa	aca	ggg	gca	aag	att	ctc	336
Leu	Glu	Glu	Thr	Lys	Gln	Gln	Leu	Glu	Lys	Thr	Gly	Ala	Lys	Ile	Leu	
			100					105					110			

gac	tac	ata	cct	gat	tat	gct	tac	att	gtc	gag	tat	gag	ggc	gat	gtt	384
Asp	Tyr	Ile	Pro	Asp	Tyr	Ala	Tyr	Ile	Val	Glu	Tyr	Glu	Gly	Asp	Val	
		115					120					125				

aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat	432
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr	
130 135 140	
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca	480
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser	
145 150 155 160	
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag	528
Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu	
165 170 175	
gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat	576
Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn	
180 185 190	
gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat	624
Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp	
195 200 205	
gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg	672
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly	
210 215 220	
ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat	720
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp	
225 230 235 240	
aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att	768
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile	
245 250 255	
act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat	816
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn	
260 265 270	
ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act	864
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr	
275 280 285	
aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg	912
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met	
290 295 300	
gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta	960
Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu	
305 310 315 320	
ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg	1008
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp	
325 330 335	
gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat	1056
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp	
340 345 350	
gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat	1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn	
355 360 365	

gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat	1152
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn	
370 375 380	
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct	1200
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser	
385 390 395 400	
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg	1248
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro	
405 410 415	
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc	1296
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe	
420 425 430	
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg	1344
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala	
435 440 445	
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca	1392
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr	
450 455 460	
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa	1440
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys	
465 470 475 480	
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att	1488
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile	
485 490 495	
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga	1536
Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly	
500 505 510	
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac	1584
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn	
515 520 525	
gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act	1632
Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr	
530 535 540	
gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc	1680
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala	
545 550 555 560	
cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt	1728
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu	
565 570 575	
gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act	1776
Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr	
580 585 590	
tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta	1824
Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val	
595 600 605	

ttt att aat gca cca caa agc ggg acg tat aca att gaa gta cag gct	1872
Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala	
610 615 620	

tat aac gta ccg gtt gga cca cag aac ttc tcg ttg gca att gtg aat	1920
Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn	
625 630 635 640	

taa	1923
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<212> PRT

<213> Bacillus sp.

<400> 8

Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
1 5 10 15

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
20 25 30

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
35 40 45

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
50 55 60

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
65 70 75 80

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
85 90 95

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
100 105 110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
115 120 125

Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
130 135 140

Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145 150 155 160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
165 170 175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
180 185 190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
195 200 205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
210 215 220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225 230 235 240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
245 250 255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
260 265 270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
275 280 285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
290 295 300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305 310 315 320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
325 330 335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
340 345 350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
355 360 365

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
370 375 380

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
 385 390 395 400

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
 405 410 415

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
 420 425 430

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
 435 440 445

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
 450 455 460

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
 465 470 475 480

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
 485 490 495

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
 500 505 510

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
 515 520 525

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
 530 535 540

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
 545 550 555 560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
 565 570 575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
 580 585 590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
 595 600 605

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
 610 615 620

Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
 625 630 635 640

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<213> Bacillus sp.

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Asn Asp Val Ala Arg His Ile Val Lys Ala Asp Val Ala Gln Ser Ser
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Tyr Gly Leu Tyr
 20

<210> 10

<211> 14

<212> PRT

<213> Bacillus sp.

<400> 10

Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
 1 5 10

<210> 11

<211> 13

<212> PRT

<213> Bacillus sp.

<400> 11

Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile Leu
 1 5 10

<210> 12

<211> 20

<212> PRT

<213> Bacillus sp.

<400> 12

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly
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Ser Tyr Ala Asp
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<210> 13

<211> 16

<212> PRT

<213> Bacillus sp.

<400> 13

Lys Asn Asp Met Val Ile Leu Phe Ala Ala Gly Asn Glu Gly Pro Asn
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<210> 14

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<220>

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<223> n is a, g, c or t

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<222> (18)..(18)

<223> n is a, g, c or t

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<223> n is a, g, c or t

<400> 14

athgtnaarg cngaygtngc ncar

24

<210> 15

<211> 23

<212> DNA

<213> Artificial/Unknown

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23

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23

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ttrcgntadt gncancncg ntgn

24

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<400> 18
athacngtng gngcnacnga raa

23

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<400> 19
ttrctrtacc antadranaa rcg

23

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21

<210> 22

<211> 21

<212> DNA

<213> Artificial/Unknown

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tctggaatct gtcgtgtagg c

21

<210> 23

<211> 20

<212> DNA

<213> Artificial/Unknown

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<223> Description of Artificial Sequence: primer

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20

<210> 24

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

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<223> Description of Artificial Sequence: primer

<400> 24

ggaggcttgc cttccaatct g

21

SEQUENCE LISTING

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<120> Alkaline Protease

<130> FP-KS-0498

<150> JP 09-274570

<151> 1997-10-07

<160> 5

<210> 1

<211> 639

<212> PRT

<213> *Bacillus sp.*

<220>

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531, 541, 584, 591, 592, 594, 595, 596, 611, 632

<223> Xaa=arbitraty amino acid

<400>

Met	Arg	Lys	Lys	Lys	Val	Phe	Leu	Ser	Val	Leu	Ser	Ala	Ala	Ala	Ile
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Leu	Ser	Thr	Val	Ala	Leu	Xaa	Asn	Pro	Ser	Ala	Gly	Xaa	Ala	Arg	Xaa
			20					25						30	
Phe	Asp	Leu	Asp	Phe	Lys	Gly	Ile	Gln	Thr	Thr	Thr	Asp	Xaa	Xaa	Gly
			35				40						45		
Phe	Ser	Lys	Gln	Xaa	Gln	Thr	Gly	Ala	Ala	Ala	Phe	Leu	Val	Glu	Ser
			50				55					60			
Glu	Asn	Val	Lys	Leu	Xaa	Lys	Gly	Leu	Xaa	Lys	Lys	Leu	Glu	Thr	Val
65				70					75					80	
Pro	Ala	Asn	Asn	Lys	Leu	His	Ile	Xaa	Gln	Phe	Asn	Gly	Pro	Ile	Leu
				85					90					95	
Glu	Glu	Thr	Lys	Gln	Xaa	Leu	Glu	Xaa	Thr	Gly	Ala	Lys	Ile	Leu	Asp
			100						105					110	
Tyr	Ile	Pro	Asp	Tyr	Ala	Tyr	Ile	Val	Glu	Tyr	Glu	Gly	Asp	Val	Xaa
			115					120					125		
Ser	Xaa	Xaa	Xaa	Xaa	Ile	Glu	His	Val	Glu	Ser	Val	Glu	Pro	Tyr	Leu
			130					135					140		
Pro	Xaa	Tyr	Xaa	Ile	Asp	Pro	Gln	Leu	Phe	Thr	Lys	Gly	Ala	Ser	Xaa
145					150					155				160	
Leu	Val	Lys	Ala	Xaa	Ala	Leu	Asp	Thr	Lys	Gln	Xaa	Asn	Lys	Glu	Val
				165						170				175	
Gln	Leu	Arg	Gly	Ile	Glu	Xaa	Ile	Ala	Gln	Xaa	Xaa	Xaa	Ser	Asn	Asp
				180					185					190	
Val	Xaa	Tyr	Ile	Thr	Ala	Lys	Pro	Glu	Tyr	Lys	Val	Met	Asn	Asp	Val
				195					200					205	

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu			
210	215	220	
Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr			
225	230	235	240
Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr			
245	250	255	
Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly			
260	265	270	
His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr Asn			
275	280	285	
Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp			
290	295	300	
Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe			
305	310	315	320
Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly			
325	330	335	
Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp			
340	345	350	
Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu			
355	360	365	
Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala			
370	375	380	
Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr			
385	390	395	400
Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr			
405	410	415	

Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa Ile

420

425

430

Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn

435

440

445

His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro

450

455

460

Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn

465

470

475

480

Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala

485

490

495

Gly Ala Ala Asp Xaa Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp

500

505

510

Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu

515

520

525

Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr Ala

530

535

540

Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro

545

550

555

560

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val

565

570

575

Ile Thr Ala Pro Asn Gly Thr Xaa Tyr Val Gly Asn Asp Phe Xaa Xaa

580

585

590

Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe

595

600

605

Ile Asn Xaa Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr

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620

Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn

625

630

635

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<211> 640

<212> PRT

<213> *Bacillus sp.*

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149, 161, 166, 173, 184, 188, 189, 190, 195, 287, 307, 325, 370, 432, 502,

532, 542, 585, 592, 593, 595, 596, 597, 612, 633

<223> Xaa=arbitrary amino acid

<400>

Met Arg Xaa Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala

1

5

10

15

Ile Leu Ser Thr Val Ala Leu Xaa Asn Pro Ser Ala Gly Xaa Ala Arg

20

25

30

Xaa Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Xaa Xaa

35

40

45

Gly Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu

50

55

60

Ser Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr

65

70

75

80

Val Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile

85	90	95
Leu Glu Glu Thr Lys Gln Xaa	Leu Glu Xaa Thr Gly Ala Lys Ile Leu	
100	105	110
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val		
115	120	125
Xaa Ser Xaa Xaa Xaa Xaa Ile Glu His Val Glu Ser Val Glu Pro Tyr		
130	135	140
Leu Pro Xaa Tyr Xaa Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser		
145	150	155
Xaa Leu Val Lys Ala Xaa Ala Leu Asp Thr Lys Gln Xaa Asn Lys Glu		
165	170	175
Val Gln Leu Arg Gly Ile Glu Xaa Ile Ala Gln Xaa Xaa Xaa Ser Asn		
180	185	190
Asp Val Xaa Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp		
195	200	205
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly		
210	215	220
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp		
225	230	235
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile		
245	250	255
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn		
260	265	270
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr		
275	280	285
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met		

290	295	300
Asp Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu		
305	310	315 320
Phe Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp		
325	330	335
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp		
340	345	350
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn		
355	360	365
Glu Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn		
370	375	380
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser		
385	390	395 400
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro		
405	410	415
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa		
420	425	430
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala		
435	440	445
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr		
450	455	460
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys		
465	470	475 480
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile		
485	490	495
Ala Gly Ala Ala Asp Xaa Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly		

500	505	510
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn		
515	520	525
Glu Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr		
530	535	540
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala		
545	550	555
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu		
565	570	575
Val Ile Thr Ala Pro Asn Gly Thr Xaa Tyr Val Gly Asn Asp Phe Xaa		
580	585	590
Xaa Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val		
595	600	605
Phe Ile Asn Xaa Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala		
610	615	620
Tyr Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn		
625	630	635
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<210> 3

<211> 1920

<212> DNA

<213> *Bacillus sp.*

<400>

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ctg	tcg	act	gtt	gca tta aac aat ccc tcg gct ggt gat gca agg act 96
Leu	Ser	Thr	Val	Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr
	20	25	30	
	ttt	gat	ctg	gat ttt aaa gga att caa aca aca acc gat gtc agt ggt 144
	Phe	Asp	Leu	Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly
	35	40	45	
	ttc	tcc	aaa	cag cga caa aca ggt gcg gct gca ttt ctg gtg gag tct 192
	Phe	Ser	Lys	Gln Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
	50	55	60	
	gaa	aat	gtg	aaa ctt ctt aaa gga ttg cta aag aaa ctt gaa aca gta 240
	Glu	Asn	Val	Lys Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val
	65	70	75	80
	ccg	gca	aat	aat aaa ctc cat att gtc caa ttc aat ggc ccc att tta 288
	Pro	Ala	Asn	Asn Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu
	85	90	95	
	gaa	gaa	aca	aaa cag aag cta gag aca act gga gca aag att ctc gac 336
	Glu	Glu	Thr	Lys Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp
	100	105	110	
	tac	atc	cct	gat tat gca tat att gtc gag tat gag ggg gat gtt cag 384
	Tyr	Ile	Pro	Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln
	115	120	125	
	tca	aaa	gtc	cgc tcc att gaa cac gtg gaa tca gtg gag cca tac ttg 432
	Ser	Lys	Val	Arg Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
	130	135	140	
	ccg	aaa	tac	aaa ata gat ccc cag ctt ttc aca aaa ggc gca tcg acg 480

Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr
 145 150 155 160
 ctg gtg aaa gcg ttg gcg ctt gat acg aag cag aac aat aaa gaa gtg 528
 Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val
 165 170 175
 caa tta aga ggc atc gag gaa atc gct cag tac gta gca agc aat gac 576
 Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp
 180 185 190
 gtc cat tat att acg gca aag cct gaa tat aag gtg atg aat gat gtg 624
 Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
 195 200 205
 gcc aga ggt att gtc aaa gcg gat gtg gca cag agc agc tac ggt ttg 672
 Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
 210 215 220
 tat gga caa ggc cag att gtc gca gtt gcc gat act gga ttg gat aca 720
 Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
 225 230 235 240
 gga aga aac gac agt tcg atg cat gaa gcc ttc cgc ggt aaa ata aca 768
 Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
 245 250 255
 gca cta tat gca ctg ggt cgg acg aat aat gcg aat gat acg aac ggt 816
 Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
 260 265 270
 cat ggt acc cat gtg gca ggt tcg gta tta gga aat ggc gca acg aat 864
 His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn
 275 280 285

aaa gga atg gca cct caa gcg aat ctg gtt ttt caa tcc atc atg gat 912
 Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
 290 295 300
 agc agt ggt ggg ctt gga ggc ttg cct tcc aat ctg caa acc tta ttc 960
 Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
 305 310 315 320
 agc caa gca ttc agt gca ggt gcc aga att cat aca aac tcc tgg ggg 1008
 Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
 325 330 335
 gca gcg gtg aat ggg gcc tac acg aca gat tcc aga aat gtg gat gac 1056
 Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
 340 345 350
 tat gta agg aaa aat gat atg acg att ctt ttc gcg gct ggg aat gaa 1104
 Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
 355 360 365
 agg ccg aac ggc ggt acc atc agt gca cct ggt acg gct aaa aac gcc 1152
 Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
 370 375 380
 ata aca gtc ggc gca acc gaa aac ctg cgt cca agc ttc ggt tcc tat 1200
 Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
 385 390 395 400
 gca gat aat att aac cac gtt gca cag ttc tct tcc cgt ggc ccg aca 1248
 Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
 405 410 415
 aaa gat ggg cga atc aag cct gat gtc atg gcg cca ggg aca tac att 1296
 Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile

420	425	430
tta tca gca aga tct tct ctt gca ccc gat tcc tcc ttc tgg gcg aat 1344		
Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn		
435	440	445
cat gac agc aaa tat gcc tat atg ggt gga acg tcc atg gca aca ccg 1392		
His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro		
450	455	460
att gtt gcg ggg aat gtt gca cag ctc cgt gag cat ttt gtg aaa aat 1440		
Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn		
465	470	475
aga gga atc act cct aag cct tcc cta ttg aaa gca gct ttg att gca 1488		
Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala		
485	490	495
ggg gct gct gat gtt gga ttg ggt tat ccg aac gga aac caa gga tgg 1536		
Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp		
500	505	510
ggc cga gtg acc ctg gat aaa tcg ttg aac gtt gcc tat gtg aac gaa 1584		
Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu		
515	520	525
tcc agt gcc cta tca act agc caa aaa gcg aca tat acc ttt act gca 1632		
Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala		
530	535	540
acg gcg ggc aag cca ttg aaa atc tcc ctg gta tgg tcg gat gcc cct 1680		
Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro		
545	550	555
gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc 1728		

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val

565

570

575

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca 1776

Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala

580

585

590

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt 1824

Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe

595

600

605

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat 1872

Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr

610

615

620

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa 1920

Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn

625

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635

<210> 4

<211> 1923

<212> DNA

<213> *Bacillus sp.*

<400>

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Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala

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10

15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg 96

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg

20	25	30	
aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa 144			
Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys			
35	40	45	
ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa 192			
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu			
50	55	60	
tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca 240			
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr			
65	70	75	80
gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att 288			
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile			
85	90	95	
tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc 336			
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu			
100	105	110	
gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt 384			
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val			
115	120	125	
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat 432			
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr			
130	135	140	
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca 480			
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser			
145	150	155	160
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag 528			

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
 165 170 175
 gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat 576
 Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
 180 185 190
 gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat 624
 Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
 195 200 205
 gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg 672
 Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
 210 215 220
 ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat 720
 Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
 225 230 235 240
 aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att 768
 Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
 245 250 255
 act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat 816
 Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
 260 265 270
 ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act 864
 Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
 275 280 285
 aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg 912
 Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
 290 295 300

gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta 960

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu

305 310 315 320

ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg 1008

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp

325 330 335

gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat 1056

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp

340 345 350

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat 1104

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn

355 360 365

gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 1152

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn

370 375 380

gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct 1200

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser

385 390 395 400

tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg 1248

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro

405 410 415

aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe

420 425 430

ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg 1344

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala

435	440	445	
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca 1392			
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr			
450	455	460	
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa 1440			
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys			
465	470	475	480
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att 1488			
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile			
485	490	495	
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga 1536			
Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly			
500	505	510	
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac 1584			
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn			
515	520	525	
gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act 1632			
Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr			
530	535	540	
gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc 1680			
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala			
545	550	555	560
cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt 1728			
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu			
565	570	575	
gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act 1776			

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr

580

585

590

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta 1824

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val

595

600

605

ttt att aat gca cca caa agc ggg acg tat aca att gag gta cag gct 1872

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala

610

615

620

tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att gtg aat 1920

Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn

625

630

635

640

taa

1923

<210> 5

<211> 1923

<212> DNA

<212> *Bacillus sp.*

<400>

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15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg 96

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg

20

25

30

aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa 144

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys	
35 40 45	
ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa	192
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu	
50 55 60	
tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca	240
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr	
65 70 75 80	
gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att	288
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile	
85 90 95	
tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc	336
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu	
100 105 110	
gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt	384
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val	
115 120 125	
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat	432
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr	
130 135 140	
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca	480
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser	
145 150 155 160	
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag	528
Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu	
165 170 175	

gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat 576
 Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
 180 185 190
 gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat 624
 Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
 195 200 205
 gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg 672
 Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
 210 215 220
 ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat 720
 Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
 225 230 235 240
 aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att 768
 Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
 245 250 255
 act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat 816
 Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
 260 265 270
 ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act 864
 Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
 275 280 285
 aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg 912
 Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
 290 295 300
 gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta 960
 Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu

305	310	315	320
ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg 1008			
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp			
325	330	335	
gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat 1056			
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp			
340	345	350	
gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat 1104			
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn			
355	360	365	
gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 1152			
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn			
370	375	380	
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct 1200			
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser			
385	390	395	400
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg 1248			
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro			
405	410	415	
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296			
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe			
420	425	430	
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg 1344			
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala			
435	440	445	
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca 1392			

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
 450 455 460
 ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa 1440
 Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
 465 470 475 480
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 485 490 495
 gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga 1536
 Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
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 Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
 515 520 525
 gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act 1632
 Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
 530 535 540
 gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc 1680
 Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
 545 550 555 560
 cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt 1728
 Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
 565 570 575
 gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act 1776
 Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
 580 585 590

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta 1824

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val

595

600

605

ttt att aat gca cca caa agc ggg acg tat aca att gaa gta cag gct 1872

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala

610

615

620

tat aac gta ccg gtt gga cca cag aac ttc tcg ttg gca att gtg aat 1920

Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn

625

630

635

640

taa

1923